# Exhibit 3

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# NiceProt View of Swiss-Prot: P41773

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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## Entry information

| | |
|---|---|
| Entry name | **LIPB_PSEFL** |
| Primary accession number | **P41773** |
| Secondary accession numbers | None |
| Entered in Swiss-Prot in | Release 32, November 1995 |
| Sequence was last modified in | Release 32, November 1995 |
| Annotations were last modified in | Release 46, February 2005 |

## Name and origin of the protein

| | |
|---|---|
| Protein name | **Lipase [Precursor]** |
| Synonyms | **EC 3.1.1.3** **Triacylglycerol lipase** |
| Gene name | None |
| From | Pseudomonas fluorescens [TaxID: 294] |
| Taxonomy | Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. |

## References

[1] NUCLEOTIDE SEQUENCE.
   STRAIN=B52;
   MEDLINE=92286777;PubMed=1599260 [NCBI, ExPASy, EBI, Israel, Japan]
   Tan Y., Miller K.J.;
   "Cloning, expression, and nucleotide sequence of a lipase gene from Pseudomonas fluorescens B52.";
   Appl. Environ. Microbiol. 58:1402-1407(1992).

## Comments

- *CATALYTIC ACTIVITY*: Triacylglycerol + $H_2O$ = diacylglycerol + a carboxylate.

- *SIMILARITY*: Belongs to the AB hydrolase superfamily. Lipase family.

## Copyright

## Cross-references

| | |
|---|---|
| EMBL | M86350; AAA25882.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] |

| PIR | A43942; A43942. |
|---|---|
| InterPro | IPR001343; Hemlysn_Ca_bind. |
| | IPR002921; Lipase_3. |
| | IPR008262; Lipase_AS. |
| | IPR000379; Ser_estrs. |
| | IPR011049; Serralysn_like_C. |
| | Graphical view of domain structure. |
| Pfam | PF00353; HemolysinCabind; 3. |
| | PF01764; Lipase_3; 1. |
| | Pfam graphical view of domain structure. |
| PRINTS | PR00313; CABNDNGRPT. |
| PROSITE | PS00330; HEMOLYSIN_CALCIUM; 1. |
| | PS00120; LIPASE_SER; 1. |
| ProDom | [Domain structure / List of seq. sharing at least 1 domain] |
| HOBACGEN | [Family / Alignment / Tree] |
| BLOCKS | P41773. |
| ProtoNet | P41773. |
| ProtoMap | P41773. |
| PRESAGE | P41773. |
| DIP | P41773. |
| ModBase | P41773. |
| SMR | P41773; FC38C080F0A3BC55. |
| SWISS-2DPAGE | Get region on 2D PAGE. |
| UniRef | View cluster of proteins with at least 50% / 90% identity. |

**Keywords**

**Hydrolase; Lipid degradation; Signal.**

**Features**

Feature table viewer

| Key | From | To | Length | Description |
|---|---|---|---|---|
| SIGNAL | 1 | 23 | 23 | Potential. |
| CHAIN | 24 | 476 | 453 | Lipase. |
| ACT_SITE | 207 | 207 | | Charge relay system (by similarity). |

**Sequence information**

Length: **476 AA** [This is the length of the unprocessed precursor]

Molecular weight: **50239 Da** [This is the MW of the unprocessed precursor]

CRC64: **FC38C080F0A3BC55** [This is a checksum on the sequence]

```
         10         20         30         40         50         60
MGIFDYKNLG TEGSKTLFAD AMAITLYSYH NLDNGFAVGY QHNGLGLGLP ATLVGALLGS

         70         80         90        100        110        120
TDSQGVIPGI PWNPDSEKAA LEAVQKAGWT PISASALGYA GKVDARGTFF GEKAGYTTAQ

        130        140        150        160        170        180
VEVLGKYDDA GKLLEIGIGF RGTSGPRETL ISDSIGDLIS DLLAALGPKD YAKNYAGEAF
```

```
        190        200        210        220        230        240
     GGLLKNVADY AGAHGLTGKD VVVSGHSLGG LAVNSMADLS NYKWAGFYKD ANYVAYASPT

        250        260        270        280        290        300
     QSAGDKVLNI GYENDPVFRA LDGSSFNLSS LGVHDKPHES TTDNIVSFND HYASTLWNVL

        310        320        330        340        350        360
     PFSIVNLPTW VSHLPTAYGD GMTRILESGF YDQMTRDSTV IVANLSDPAR ANTWVQDLNR

        370        380        390        400        410        420
     NAEPHKGNTF IIGSDGNDLI QGGNGADFIE GGKGNDTIRD NSGHNTFLFS GHFGNDRVIG

        430        440        450        460        470
     YQPTDKLVFK DVQGSTDLRD HAKVVGADTV LTFGADSVTL VGVGHGGLWT EGVVIG
```

P41773 in FASTA
format

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**BLAST**  BLAST submission on
ExPASy/SIB
or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

ScanProsite, MotifScan

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